10/586374 SEQUENCE LASP20 Rec'd PCT/PTO 14 JUL 2006

Xiaotian Zhong <120> Coccidian parasite casein kinase I as a chemotherapeutic target for antiprotozoal agents <130> 21554P <150> 60/537,094 <151> 2004-01-16 <150> PCT/US2005/000955 <151> 2005-01-12 <160> 45 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 2182 <212> DNA <213> Eimeria tenella <220> <221> CDS <222> (715) ... (1722) <400> 1 geggeegegt egaegtettt getgeegeae agggageage ageageegee gaeeegatee 60 cttgggagcc caccaagtgc tgcgcttgct tagcagctac aggagctgcc gcggggttgc 120 tccctgaggc agcgtgcatg tatggtccgg cagccagctt ggtgtcgcag ccgtacttct 180 tggaagcgag agagactgtg ggagagcgca aatcactcca gccgcttcca ggggagtctg 240 gggaccgcag gagcgttgga ggctgcctgc cggcataaac aggaacaagc gcattcttat 300 tcttctgtgg ttgctgagtt ctggctgcgt tcaagggggt tcacctcttc cccttctggc 360 acgcggtgca ccttttacgt aagagcgtcg atagcatcgg tcatctacag cagcgtgctg 480 ctgcttccgt gacctttaca ctgcttgtgg cgggccgtct tgtagagggg ccatctgctt 540 gttcgctgct ggacgcagac ccggcgcccg acatttccgg cagccgggca gttgagataa 600 accggctgcc cggtggccgt cgaaattgaa gcaggatctc tacagtaagg aacaaatcgc 660 gctattttta aggagtgtgt atacttgggg cgttactcgt gagtattgct gatg atg 717 Met 1 765 gac gtc cgt gtg ggg ggt aag tat cgt ttg ggg agg aag att ggg agc Asp Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser 10 15 gga tcc ttc ggc gac atc tac ctt ggt acg aac atc tca aca gga gat 813 Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asn Ile Ser Thr Gly Asp 25 30 20

<110> Robert G.K. Donald

Paul Liberator

861

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1236

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Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu
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Gly Arg Lys Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Lys Gly Leu Asn Ser Gln Thr Gly Gln Glu Val Ala Leu Lys Val Glu Ser Thr Lys Ala Lys His Pro Gln Leu Leu Tyr Glu Tyr Lys Leu Leu Lys His Leu Gln Gly Gly Thr Gly Ile Ala Gln Val Phe Cys Cys Glu Thr Ala Gly Asp His Asn Ile Met Ala Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Val Phe Asn Leu Cys Asn Arg Thr Phe Ser Leu Lys Thr Ile Leu Leu Leu Ala Asp Gln Phe Leu Gln Arg Val Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp Ile Lys Pro Asp Asn Phe Leu Leu Gly Gly Ala Gly Asn Gln Asn Thr Ile Tyr Val Ile Asp Phe Gly Leu Ala Lys Lys Phe Arg Asp Pro Lys Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Ile Ser Ala His Leu Gly Ser Glu Gln Ser Arg Arg Asp Asp Leu Glu Ala Val Gly Tyr Val Leu Met Tyr Phe Cys Arg Gly Gly Thr Leu Pro Trp Gln Gly Ile Lys Ala Asn Thr Lys Gln Glu Lys Tyr His Lys Ile Met Glu Lys Lys Met Ser Thr Pro Val Glu Val Leu Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr Tyr Leu His Tyr Cys Arg Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Lys Arg Leu Phe Arg Asp Leu Tyr Ile Lys Glu Gly Tyr 290 295 300 Asp Asp Ser Asp Arg Glu Phe Asp Trp Thr Val Lys Leu Ser Ser Arg Ser Leu Gly Pro Pro Ser Ser Arg Ala Gln His Val Leu Leu Ser Gln Asp Thr Arg Thr Arg Gly Lys Arg Glu Thr Asp Arg Pro Val Ala Ala Arg Ser Gly Asp Arg Glu Arg Gly Ile His Phe Ser Asn Gly Asn Val Gly Asn Pro Ser Met Ala Thr Asn Pro Gly Gly Leu Ser Val Met Val His Glu Arg Thr Ser Leu Val Asp Gln Gly Asp Arg Gly Ser Arg Glu Thr Ser Thr Arg Lys Glu Asp Ala Lys Asp Gly Arg Trp Pro Gly Gly Arg Phe Ser Cys Leu Pro Leu Leu Cys Arg Arg Ser Pro Thr Lys Ala

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aggaccgacc ggactacgcc tacctcaagc gactctttcg agatctctac atcaaagagg 480
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atgacagtga ccgcgaattc gactggacag tgaaactttc gtcgcgcagt ctcggaccgc 180
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<400> 11

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                                                45
Leu Leu Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Gly Gly Gly Ile Gly
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                        55
Val Pro Lys Val Tyr Trp Tyr Gly Ile Glu Gly Asp Phe Thr Ile Met
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Val Leu Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Thr Leu Cys
                                                        95
                                    90
                85
Asn Arg Lys Phe Ser Leu Lys Thr Val Arg Met Thr Ala Asp Gln Met
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Leu Asn Arg Ile Glu Tyr Val His Ser Lys Asn Phe Ile His Arg Asp
       115 120 125
Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Val Thr Leu
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Ile His Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ser Arg
145
                    150
                                        155
                                                            160
Ser His Thr Ser Tyr Pro Tyr Lys Glu Gly Lys Asn Leu Thr Gly Thr
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                                    170
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Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
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Arg Asp Asp Ile Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Leu Arg
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                                                205
Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ile Ser Lys Lys Asp Lys
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Tyr Asp Lys Ile Met Glu Lys Lys Ile Ser Thr Ser Val Glu Val Leu
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Cys Arg Asn Ala Ser Phe Glu Phe Val Thr Tyr Leu Asn Tyr Cys Arg
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                                    250
                                                        255
Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Thr Tyr Leu Arg Arg Leu
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Gln Arg Asn Asn

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Gln Glu Gln Gln Ser Phe Pro Gly Gly Ser Asn Gly Gly Gly Ala Ala

Gly Asn Gly Ser Pro Val Asn Gln Ser Pro Ala Gln Gly Gly Asn Gly 325 330 335
Gly Ala Pro Asn Ser Ala Asn Asn Gln Glu Ser Gly Ala Pro Glu Gln 340 345 350
Gln

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<213> Trypanosoma cruzi

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Gln Arg Glu Arg Gly Asp Val Glu Gln Ala 325 330

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